WHAT IS CLAIMED IS:

1	1. A method of identifying the biological function of a candidate
2	gene, the method comprising the steps of:
3	(i) selecting a first candidate gene;
4	(ii) providing a first zinc finger protein that binds to a first target site of the
5	first candidate gene and a second zinc finger protein that binds to a target site of a second
6	gene;
7	(iii) culturing a first cell under conditions where the first zinc finger
8	protein contacts the first candidate gene and culturing a second cell under conditions
9	where the second zinc finger protein contacts the second candidate gene, wherein the first
0	and the second zinc finger proteins modulate expression of the first and second candidate
11	genes; and
12	(iv) assaying for a selected phenotype, thereby identifying whether or not
13	the first candidate gene is associated with the selected phenotype.
	2. The method of claim 1, further comprising providing a third zinc
1	2. The method of claim 1, further comprising providing a third zinc finger protein that binds to a second target site of the first candidate gene.
2	ringer protein that binds to a second target site of the first candidate gene.
1	The method of claim 1, further comprising selecting a plurality of
2	candidate genes and providing a plurality of zinc finger proteins that bind to a target site
3	of each candidate gene.
1	4. The method of claim 1, wherein the second gene is a control gene.
1	4. The method of claim 1, wherein the second gene is a control gene.
1	5. The method of claim 1, wherein the first candidate gene is partially
2	encoded by an EST of at least about 200 nucleotides in length.
	The state of the s
1	6. The method of claim 1, wherein the first candidate gene and the
2	second gene are both associated with the selected phenotype.
1	7. The method of claim 1, wherein the first and second cell are the
2	same cell, wherein the cell comprises the first and second candidate genes.
1	8. The method of claim 1, wherein the first and the second candidate
2	genes are endogenous genes.

1	9.	The method of claim 1, wherein expression of the candidate genes
2	is inhibited by at leas	t about 50%.
1	10.	The method of claim 1, wherein expression of the candidate genes
2	is activated by at leas	
	•	
1	11.	The method of claim 1, wherein the zinc finger proteins are fusion
2	proteins comprising	a regulatory domain.
1	12.	The method of claim 1, wherein expression of the zinc finger
,2	proteins is induced by	y administration of an exogenous agent.
•	12	The method of claim 11, wherein the zinc finger proteins are fusion
1	13.	at least two regulatory domains.
2 .	proteins comprising	at least two regulatory domains.
1	14.	The method of claim 1, wherein the cell is selected from the group
2	consisting of animal	cell, a plant cell, a bacterial cell, a protozoal cell, or a fungal cell.
1	15.	The method of claim 14, wherein the cell is a mammalian cell
1	16.	The method of claim 15, wherein the cell is a human cell
1	17.	The method of claim 1, wherein the modulation of expression is
2	activation of gene ex	pression that prevents repression of gene expression.
1	18.	The method of claim 1, wherein the modulation of expression is
2	inhibition of gene ex	pression that prevents gene activation.
1	19.	The method of claim 11, wherein the regulatory domain is selected
2		isting of a transcriptional repressor, a methyl transferase, a
3	transcriptional activa	ator, a histone acetyltransferase, and a histone deacetylase.
1	20.	The method of claim 1, wherein the first and second zinc finger
2	proteins are encoded	by an expression vector comprising a zinc finger protein nucleic
3	acid operably linked	to a promoter, and wherein the method further comprises the step of
4	first administering th	he expression vector to the cell.

21. T	he method of claim 20, wherein expression of the zinc finger
proteins is under small	molecule control.
22. T	The method of claim 21, wherein expression of the first zinc finger
protein and expression	of the second zinc finger protein are under different small
•	ein both the first and the second zinc finger protein are fusion
	egulatory domain, and wherein the first and the second zinc finger
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23.	The method of claim 22, wherein both the first and the second zinc
finger proteins compris	e a regulatory domain that represses gene expression.
24.	The method of claim 20, wherein the expression vector is a viral
vector.	
25.	The method of claim 24, wherein the expression vector is a
	ector, an adenoviral expression vector, or an AAV expression
vector.	
26.	The method of claim 20, wherein the zinc finger proteins are
	cid operably linked to an inducible promoter.
	The method of claim 1, wherein the cell comprises less than about
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28.	The method of claim 1, wherein the target site is upstream of a
transcription initiation	site of the candidate gene.
29.	The method of claim 1, wherein the target site is adjacent to a
transcription initiation	site of the candidate gene.
30.	The method of claim 1, wherein the target site is adjacent to an
RNA polymerase paus	se site downstream of a transcription initiation site of the candidate
gene.	
31.	A method of identifying the biological function of a candidate
gene, the method com	
	proteins is under small and 22. The protein and expression of molecule control, where proteins comprising a reproteins are expressed in 23. The finger proteins comprise 24. The vector. 25. The retroviral expression vector. 26. The encoded by a nucleic and 27. The standard copies of each 28. The transcription initiation 29. The transcription initiation 30. RNA polymerase pausingene.

3	(1) identifying a plurality of calididate genes,		
4	(ii) providing a first zinc finger protein that binds to a first target site of a		
5	first candidate gene;		
6	(iii) culturing a first cell under conditions where the first zinc finger		
7	protein contacts the first candidate gene, wherein the first zinc finger protein modulates		
8	expression of the first candidate gene;		
9	(iv) determining the expression pattern of the candidate genes and		
10	determining whether or not the first candidate gene is associated with the selected		
11	phenotype; and		
12	(v) repeating steps (ii)-(iv) for each candidate gene.		
1	32. The method of claim 31, further comprising providing a second		
2	zinc finger protein that binds to a second target site of the first candidate gene.		
1	33. The method of claim 31, wherein at least one of the candidate		
2	genes is an EST of at least about 200 nucleotides in length.		
1	34. The method of claim 31, wherein at least two candidate genes are		
2	required to cause the selected phenotype.		
1	35. The method of claim 31, wherein the candidate genes are		
2	endogenous genes.		
1	36. The method of claim 31, wherein expression of the candidate gene		
2	is inhibited by at least about 50%.		
1	37. The method of claim 31, wherein expression of the candidate gene		
2	is activated to at least about 150%.		
1	38. The method of claim 31, wherein the zinc finger protein is a fusion		
2	protein comprising a regulatory domain.		
1	39. The method of claim 38, wherein the regulatory domain is under		
2	small molecule control.		
1	40. The method of claim 38, wherein the zinc finger proteins are fusion		
2	proteins comprising at least two regulatory domains.		

1		41.	The method of claim 31, wherein the cell is selected from the
2	group consistin	ng of an	imal cell, a plant cell, a bacterial cell, a protozoal cell, or a fungal
3	cell.		
1		42.	The method of claim 41, wherein the cell is a mammalian cell
1		43.	The method of claim 42, wherein the cell is a human cell
1		44.	The method of claim 31, wherein the modulation of expression is
2	activation of ge	ene exp	pression that prevents repression of gene expression.
1		45.	The method of claim 31, wherein the modulation of expression is
2	inhibition of ge	ene exp	pression that prevents gene activation.
1		46.	The method of claim 38, wherein the regulatory domain is selected
2	from the group	consis	sting of a transcriptional repressor, a methyl transferase, a
3			or, a histone acetyltransferase, and a histone deacetylase.
1		47.	The method of claim 31, wherein the zinc finger protein is encoded
2	by an expressi	on vect	or comprising a zinc finger protein nucleic acid operably linked to a
3			n the method further comprises the step of first administering the
4	expression vec		
1		48.	The method of claim 47, wherein expression of the zinc finger
2	protein is unde	er smal	l molecule control.
1		49.	The method of claim 47, wherein the expression vector is a viral
2	vector.		
1		50.	The method of claim 49, wherein the expression vector is a
2	retroviral expr	ression	vector, an adenoviral expression vector, or an AAV expression
3	vector.		
1		51.	The method of claim 47, wherein the zinc finger protein is encoded
2	by a nucleic a	cid ope	rably linked to an inducible promoter.
1		52.	The method of claim 31, wherein the cell comprises less than abou

1.5x10⁶ copies of the zinc finger protein.

1	53. The method of claim 31, wherein the target site is up	stream of a	
2	transcription initiation site of the candidate gene.		
1	54. The method of claim 31, wherein the target site is ac	ljacent to a	
2 -	transcription initiation site of the candidate gene.		
1	55. The method of claim 31, wherein the target site is ac	ljacent to an	
2	RNA polymerase pause site downstream of a transcription initiation site of	the candidate	
3	gene.		
.1	56. A method of identifying the biological function of a	candidate	
2	gene, the method comprising the steps of:		
3	(i) selecting a first candidate gene;		
4	(ii) providing a first zinc finger that binds to a first target sit	e of the first	
5	candidate gene and a second zinc finger that binds to a second target site o	f the first	
6			
7	(iii) culturing a first cell under conditions where the first zing	nc finger	
8			
9			
10			
11			
12			
1	The method of claim 56, further comprising providi	ng a third zinc	
2	finger protein that binds to a target site of a second candidate gene.		
1	1 58. The method of claim 56, further comprising selecting	ıg a plurality of	
2	candidate genes and providing a plurality of zinc finger proteins that bind	to a target site	
3	of each candidate gene.		
1	1 59. The method of claim 57, wherein the second candid	ate gene is a	
2	2 control gene.		
1	1 60. The method of claim 56, wherein the first candidate	gene is an EST	
2	of at least about 200 nucleotides in length.		

1	61.	The method of claim 57, wherein the first candidate gene and the
2	second candidate ger	ne are both required for causing the selected phenotype.
1	62.	The method of claim 56, wherein the first and second cell are the
2	same cell.	. '
1	63.	The method of claim 56, wherein the first candidate gene is an
2	endogenous gene.	
1	64.	The method of claim 56, wherein expression of the first candidate
,2	gene is inhibited by	
1	65.	The method of claim 56, wherein expression of the first candidate
2	gene is activated to a	
1	66.	The method of claim 56, wherein the first zinc finger protein is a
1 2		rising a regulatory domain.
1	67	The method of claim 66, wherein the regulatory domain is under
1 2	67. small molecule cont	
_		
1	68.	The method of claim 66, wherein the zinc finger proteins are fusion
2	proteins comprising	at least two regulatory domains.
1	69.	The method of claim 56, wherein the cell is selected from the
2	group consisting of	animal cell, a plant cell, a bacterial cell, a protozoal cell, or a fungal
3	cell.	
1	70.	The method of claim 69, wherein the cell is a mammalian cell
1	71.	The method of claim 71, wherein the cell is a human cell
1	72.	The method of claim 56, wherein the modulation of expression is
2	activation of gene e	xpression that prevents repression of gene expression.
1	73.	The method of claim 56, wherein the modulation of expression is
2	inhibition of gene e	enression that prevents gene activation.

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1	74.	The method of claim 66, wherein the regulatory domain is selected
2	from the group consis	ting of a transcriptional repressor, a methyl transferase, a
3	transcriptional activat	or, a histone acetyltransferase, and a histone deacetylase.
	7.5	The method of claim 56, wherein the first and the second zinc
1	75.	
2	-	coded by an expression vector comprising a zinc finger protein
3		linked to a promoter, and wherein the method further comprises the
4	step of first administe	ring the expression vector to the cell.
1	76.	The method of claim 75, wherein expression of the zinc finger
`2	proteins is under sma	ll molecule control.
1	77.	The method of claim 76, wherein expression of the first zinc finger
2		n of the second zinc finger protein are under different small
3	=	erein both the first and the second zinc finger protein are fusion
4		regulatory domain, and wherein the first and the second zinc finger
	proteins are expressed	
5	proteins are expressed	in the same con.
1	78.	The method of claim 77, wherein the first zinc finger protein
2	comprises a regulator	y domain that represses gene expression and the second zinc finger
3	protein comprises a r	egulatory domain that activates gene expression.
	5 0	The state of the second of the expression vector is a viral
1	79.	The method of claim 75, wherein the expression vector is a viral
2	vector.	
1	80.	The method of claim 79, wherein the expression vector is a
2	retroviral expression	vector, an adenoviral expression vector, or an AAV expression
3	vector.	
	21	The method of claim 75, wherein the zinc finger proteins are
1	81.	
2	encoded by a nucleic	acid operably linked to an inducible promoter.
1	82.	The method of claim 56, wherein the cell comprises less than about
2	1.5x10 ⁶ copies of eac	ch zinc finger protein.
_	22	The state of the state of the first or the second torget site
1	83.	The method of claim 56, wherein the first or the second target site

is upstream of a transcription initiation site of the first candidate gene.

1	84. The method of claim 56, wherein the first or the second target site		
2	is adjacent to a transcription initiation site of the first candidate gene.		
1	85. The method of claim 56, wherein the first or the second target site		
2	is adjacent to an RNA polymerase pause site downstream of a transcription initiation site		
3	of the first candidate gene.		
1			
1	86. A method of identifying the biological function of a candidate		
2	gene, the method comprising the steps of:		
3	(i) selecting a first candidate gene;		
`4	(ii) providing a first zinc finger protein that binds to a first target site of the		
5	first candidate gene;		
6	(iii) culturing a first cell under conditions where the first candidate zinc		
7	finger protein contacts the first candidate gene, wherein the first zinc finger proteins		
8	modulate expression of the first candidate gene; and		
9	(iv) assaying for a selected phenotype, thereby identifying whether or not		
10	the first candidate gene is associated with the selected phenotype.		